Claims

1. A peptide having sequence and structural duality that can reversibly switch between a first structural form that can oligomerise and a second monomeric structural form in response to a stimulus, wherein the peptide comprises interactive motifs that interact to form a bond in response to the stimulus and thereby cause the peptide to assume the second structural form.

2. A peptide having sequence and structural duality which can reversibly switch between a first structural form and a second structural form in response to a stimulus, wherein the peptide comprises interactive motifs that interact to form a bond in response to the stimulus and thereby cause the peptide to assume the second structural form, wherein the peptide does not switch between an α helical structure and a β sheet structure.

3. The peptide according to claim 1 or claim 2, wherein the peptide forms a continuous helical structure as the first structural form.

4. The peptide according to claim 3, wherein the first structural form of the peptide can oligomerise.

5. The peptide according to claim 4, wherein the first structural form of the peptide dimerises to form a parallel coiled-coil dimer.

6. The peptide according to any one of the previous claims, wherein the peptide forms a hairpin structure as the second structural form.

7. The peptide according to claim 6, wherein the second structural form of the peptide is an antiparallel coiled-coil monomer.

8. The peptide according to any one of the preceding claims, wherein the peptide has two different superimposed sequence and structural motifs.

9. The peptide according to claim 8, wherein the first sequence motif is a coiled-coil motif for a parallel coiled-coil dimer structure.

10. The peptide according to claim 8 or claim 9, wherein the second sequence motif is a coiled-coil motif for an antiparallel coiled-coil monomer structure.

11. The peptide according to any one of the preceding claims, wherein the interactive motifs form a covalent or non-covalent bond in response to a stimulus.

12. The peptide according to claim 11, wherein the interactive motifs are cysteine residues which form a di-sulphide linkage in response to an oxidising environment.

13. The peptide according to claim 11, wherein the interactive motifs comprise parts of a metal binding site which form a non-covalent linkage in the presence of a corresponding metal ion.

14. The peptide according to claim 11, wherein the interactive motifs comprise parts of an antigen binding site of an antibody molecule which form a non-covalent linkage in the presence of the corresponding antigen.

15. The peptide according to claim 11, wherein the interactive motifs comprise parts of a ligand binding site of a receptor which form a non-covalent linkage in the presence of the corresponding ligand.

16. The peptide according to claim 12, having the following sequence:

X^1 -$(Y)_n$- $(abcdefg)_m$-*abcdef*$((Z)_p)$*g*-$(abcdefg)_m$-*abcde*-$(Y)_n$-X^2

wherein:

X^1 and X^2 are motifs capable of interacting to form a bond;

Y is any amino acid capable of acting as a linker;

$_n$ is independently selected form 0 to 20;

abcdefg is a heptad sequence motif;

$_m$ is 1 to 20;

abcde is the first 5 residues of a heptad sequence motif;

Z is an amino acid that is compatible with the 2 structural forms of the peptide; and

$_p$ is 1 to 6.

17. The peptide according to claim 16, wherein X^1 and X^2 are an amino acid capable of forming a disulphide link.

18. The peptide according to claim 17, wherein X^1 and X^2 are cysteine.

19. The peptide according to any one of claims 16 to 18, wherein Y is independently selected from glycine, serine or β-alanine.

20. The peptide according to any one of claims 16 to 19, wherein the *d* of the heptad sequence is leucine

21. The peptide according to any one of claims 16 to 20, wherein the *a* of the heptad sequence is independently selected from isoleucine, valine, lysine, asparagine and arginine, provided *a* is lysine, asparagine or arginine in only 1 in every 4 heptad sequences of the peptide.

22. The peptide according to any one of claims 16 to 20, wherein the *a* of the heptad sequence is isoleucine or lysine provided *a* is only lysine in one of the heptad sequences of the peptide.

23. The peptide according to any one of claims 16 to 20, wherein the *g* and *e* of the heptad repeat are oppositely charged and the polarity of the *g* and *e* are reversed in the C-terminal half of the peptide compared to the N-terminal half of the peptide.

24. The peptide according to any one of claims 16 to 22, wherein Z is independently selected from glycine, alanine and glutamine.

25. The peptide according to any one of claims 16 to 23, wherein $(Z)_p$ is Ala-Lys-Gln-Ala; or Ala-Ala-Gln-Ala.

26. The peptide according to claim 12, wherein the peptide has the following sequence:

CGGEIRALKYEIARLKQAKQAKIRALEQKIAALEGGC;

CGGEIRALKYEIARLKQAAQAKIRALEQKIAALEGGC; or

CGGEIRALKYEIARLKQAAQAKKRALEQKIAALEGGC.

27. Use of the peptide according to any one of the preceding claims for determining the presence or absence of a stimulus.

28. A method of detecting a stimulus comprising incubating a peptide according to any one of claims 1 to 26 with a test solution, and determining if the peptide has the first structural form or the second structural form in the test solution, wherein if the peptide assumes the second structural form, the test solution contains the stimulus.

29. A method for constructing a peptide that has sequence and structural duality, which can reversibly switch between a first and a second structural form in response to a stimulus, comprising:

(i) designing and producing a peptide using sequence rules for the first and second structural forms, wherein the sequence rules are superimposed in the peptide; and

(ii) providing interactive motifs in the peptide that form a bond in response to a stimulus, wherein the bond stabilises the second structural form, and wherein in the absence of the bond the second structural form is not stabilised and the peptide preferentially forms the first structural form.

30. The method of claim 29, for constructing the peptide according to any one of claims 1 to 26.